10/622,182

	ENTRY	SESSION
FULL ESTIMATED COST	29.80	30.01

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=> file biosis medline caplus wpids uspatfull
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COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	30.24	30.45

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*** YOU HAVE NEW MAIL ***

=> s mass tag and dna
L6         282 MASS TAG AND DNA

=> s l6 and dna fragments
   3 FILES SEARCHED...
L7          59 L6 AND DNA FRAGMENTS

=> s l7 and cleav? (5a) tag
L8          33 L7 AND CLEAV? (5A) TAG

=> s l8 and charge
L9          27 L8 AND CHARGE

=> s l9 and mass spectrometry
L10         27 L9 AND MASS SPECTROMETRY

=> dup rem l10
PROCESSING COMPLETED FOR L10
L11          27 DUP REM L10 (0 DUPLICATES REMOVED)

=>  s l11 and actinic
L12          1 L11 AND ACTINIC

=> d l12 bib abs

L12  ANSWER 1 OF 1  USPATFULL on STN
AN     2002:322437  USPATFULL
TI     Method and reagents for analyzing the nucleotide sequence of nucleic
       acids
IN     Sampson, Jeffrey R., Burlingame, CA, UNITED STATES
       Myerson, Joel, Berkeley, CA, UNITED STATES
       Tsalenko, Anna M., Chicago, IL, UNITED STATES
       Sampas, Nicholas M., San Jose, CA, UNITED STATES
       Webb, Peter G., Menlo Park, CA, UNITED STATES
       Yakhini, Zohar H., Zikhron Ya'Acov, ISRAEL
PI     US 2002182601      A1   20021205
AI     US 2001-836012     A1   20010417 (9)
RLI    Continuation-in-part of Ser. No. US 1998-112437, filed on 9 Jul 1998,
```

GRANTED, Pat. No. US 6218118
DT Utility
FS APPLICATION
LREP AGILENT TECHNOLOGIES, Legal Department, DL429, Intellectual Property Administration, P.O. Box 58043, Santa Clara, CA, 95052-8043
CLMN Number of Claims: 80
ECL Exemplary Claim: 1
DRWN 13 Drawing Page(s)
LN.CNT 3253
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods and reagents are disclosed which provide for more sensitive, more accurate and higher through-put analyses of target nucleic acid sequences. The methods and reagents of the present invention may be generically applied to generally any target nucleic acid sequence and do not require a priori information about the presence, location or identity of mutations in the target nucleic acid sequence. The reagents of the invention are mixtures of oligonucleotide precursors having a high level of coverage and mass number complexity, and also having tags analyzable by mass spectrometry which are covalently linked to the precursors through cleavable bonds. A method is also disclosed for analyzing a target nucleic acid sequence employing the mixtures of oligonucleotide precursors having tags analyzable by mass spectrometry covalently linked to the oligonucleotide precursors through cleavable bonds, and chemical or enzymatic assays to alter the mass of the oligonucleotide precursors prior to mass spectral analysis. The enzymatic assay may be a polymerase extension assay or a ligation-based assay. The kits for carrying out the methods of the invention are also disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=>

=> file reg
COST IN U.S. DOLLARS

	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	47.94	78.39

FILE 'REGISTRY' ENTERED AT 12:32:23 ON 24 OCT 2006
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STRUCTURE FILE UPDATES: 23 OCT 2006 HIGHEST RN 911100-17-9
DICTIONARY FILE UPDATES: 23 OCT 2006 HIGHEST RN 911100-17-9

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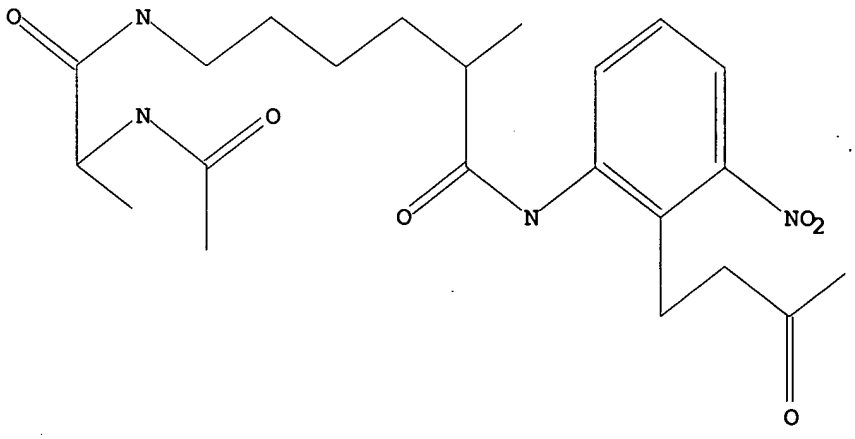
L13 STRUCTURE UPLOADED

=> d l13
L13 HAS NO ANSWERS
L13 STR



Structure attributes must be viewed using STN Express query preparation.

=> s l13 full
FULL SEARCH INITIATED 12:32:48 FILE 'REGISTRY'
FULL SCREEN SEARCH COMPLETED - 2 TO ITERATE

100.0% PROCESSED 2 ITERATIONS 0 ANSWERS
SEARCH TIME: 00.00.01

L14 0 SEA SSS FUL L13

=>

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>
=>  his
HIS IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> d his

     (FILE 'HOME' ENTERED AT 12:04:28 ON 24 OCT 2006)

     FILE 'REGISTRY' ENTERED AT 12:05:02 ON 24 OCT 2006
L1             0 S 1-METHYPIPERIDINE-4-CARBALDEHYDE/CN
L2             0 S 1-METHYPIPERIDINE/CN
L3             0 S 1-METHYLPIPERIDINE-4-CARBALDEHYDE/CN
L4            25 S 1-METHYLPIPERIDIN?/CN
                 E 1-METHYLPIPERIDINE-4-CARBALDEHYDE/CN
L5             1 S E4

     FILE 'BIOSIS, MEDLINE, CAPLUS, WPIDS, USPATFULL' ENTERED AT 12:14:50 ON
     24 OCT 2006
L6           282 S MASS TAG AND DNA
L7            59 S L6 AND DNA FRAGMENTS
L8            33 S L7 AND CLEAV? (5A) TAG
L9            27 S L8 AND CHARGE
L10           27 S L9 AND MASS SPECTROMETRY
L11           27 DUP REM L10 (0 DUPLICATES REMOVED)
L12            1 S L11 AND ACTINIC

     FILE 'REGISTRY' ENTERED AT 12:32:23 ON 24 OCT 2006
L13              STRUCTURE UPLOADED
L14            0 S L13 FULL

=> d l11 bib abs 1-27
YOU HAVE REQUESTED DATA FROM FILE 'USPATFULL' - CONTINUE? (Y)/N:y



L11  ANSWER 1 OF 27  USPATFULL on STN
AN     2006:86484  USPATFULL
TI     Mass defect labeling for the determination of oligomer sequences
IN     Schneider, Luke V., Half Moon Bay, CA, UNITED STATES
       Hall, Michael P., San Carlos, CA, UNITED STATES
       Petesch, Robert, Newark, CA, UNITED STATES
PA     Taget Discovery, Inc., Palo Alto, CA, UNITED STATES (U.S. corporation)
PI     US 2006073485      A1   20060406
AI     US 2004-913020     A1   20040806 (10)
RLI    Continuation of Ser. No. US 2001-35349, filed on 19 Oct 2001, GRANTED,
       Pat. No. US 6962818
PRAI   US 2000-242165P     20001019 (60)
       US 2000-242398P     20001019 (60)
DT     Utility
FS     APPLICATION
LREP   TOWNSEND AND TOWNSEND AND CREW, LLP, TWO EMBARCADERO CENTER, EIGHTH
       FLOOR, SAN FRANCISCO, CA, 94111-3834, US
CLMN   Number of Claims: 19
ECL    Exemplary Claim: 1-50
DRWN   32 Drawing Page(s)
LN.CNT 3323
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     Mass tagging methods are provided that lead to mass spectrometer
       detection sensitivities and molecular discriminations that are improved
       over other methods. In particular the methods are useful for
       discriminating tagged molecules and fragments of molecules from chemical
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noise in the mass spectrum. These mass tagging methods are useful for oligomer sequencing, determining the relative abundances of molecules from different samples, and identifying individual molecules or chemical processing steps in combinatorial chemical libraries. The methods provided are useful for the simultaneous analysis of multiple molecules and reaction mixtures by mass spectrometric methods.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 2 OF 27 USPATFULL on STN
AN 2005:247630 USPATFULL
TI Multiplex sample analysis on universal arrays
IN Stuelpnagel, John, Encinitos, CA, UNITED STATES
PI US 2005214825 A1 20050929
AI US 2005-36886 A1 20050114 (11)
RLI Continuation-in-part of Ser. No. US 2003-620852, filed on 15 Jul 2003, PENDING Continuation-in-part of Ser. No. US 2002-194958, filed on 12 Jul 2002, PENDING Continuation-in-part of Ser. No. US 2002-177727, filed on 20 Jun 2002, PENDING Continuation-in-part of Ser. No. US 2001-931285, filed on 16 Aug 2001, GRANTED, Pat. No. US 6913884 Continuation-in-part of Ser. No. US 2001-915231, filed on 24 Jul 2001, GRANTED, Pat. No. US 6890741 Continuation-in-part of Ser. No. US 2001-779376, filed on 7 Feb 2001, PENDING Continuation-in-part of Ser. No. WO 2001-US4056, filed on 7 Feb 2001, PENDING
PRAI US 2002-396237P 20020715 (60)
US 2001-341827P 20011217 (60)
US 2001-336958P 20011203 (60)
US 2001-311271P 20010809 (60)
US 2001-305118P 20010712 (60)
US 2001-297609P 20010611 (60)
US 2000-234143P 20000921 (60)
US 2000-234732P 20000922 (60)
US 2000-180810P 20000207 (60)
US 2000-234732P 20000922 (60)
US 2000-180810P 20000207 (60)
DT Utility
FS APPLICATION
LREP David A. Gay, McDermott Will & Emery LLP, Suite 700, 4370 La Jolla Village Drive, San Diego, CA, 92122, US
CLMN Number of Claims: 52
ECL Exemplary Claim: 1
DRWN 29 Drawing Page(s)
LN.CNT 6246
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides a method of identifying at least one target sequence in each sample of a plurality of samples. The method includes the steps of (a) contacting at least one target sequence within a plurality of separate samples each with a nucleic acid probe under conditions wherein the probes form hybridization complexes with the at least one target sequence, wherein each of the probes has the same target specific sequence and a different adapter sequence that is unique to a separate sample; (b) pooling the probes thereby forming a probe pool; and (c) detecting the presence of the adapter sequence in the probe pool, thereby identifying the at least one target sequences in each sample of the plurality of separate samples.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 3 OF 27 USPATFULL on STN
AN 2005:30749 USPATFULL
TI Direct multiplex characterization of genomic DNA
IN Willis, Thomas D., San Francisco, CA, UNITED STATES
Hardenbol, Paul, Los Altos, CA, UNITED STATES
Jain, Maneesh, Menlo Park, CA, UNITED STATES

Stolc, Viktor, Cupertino, CA, UNITED STATES
Ronaghi, Mostafa, Palo Alto, CA, UNITED STATES
Davis, Ronald W., Palo Alto, CA, UNITED STATES
PA The Board of Trustees of the Leland Stanford Junior University, Palo Alto, CA (U.S. corporation)
PI US 2005026180 A1 20050203
AI US 2004-826633 A1 20040415 (10)
RLI Continuation of Ser. No. US 2001-999362, filed on 24 Oct 2001, PENDING
PRAI US 2000-242901P 20001024 (60)
DT Utility
FS APPLICATION
LREP FISH & NEAVE LLP, 1251 AVENUE OF THE AMERICAS, 50TH FLOOR, NEW YORK, NY, 10020-1105
CLMN Number of Claims: 2
ECL Exemplary Claim: 1
DRWN 18 Drawing Page(s)
LN.CNT 4224
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention is directed to novel methods of multiplexing nucleic acid reactions, including amplification, detection and genotyping. The invention relies on the use of precircle probes that are circularized in the presence of the corresponding target nucleic acids, cleaved, and then amplified.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 4 OF 27 USPATFULL on STN
AN 2004:334806 USPATFULL
TI Binary encoded sequence tags
IN Kaufman, Joseph C., Hamden, CT, UNITED STATES
Roth, Matthew E., Branford, CT, UNITED STATES
Lizardi, Paul M., Wallingford, CT, UNITED STATES
Feng, Li, Hamden, CT, UNITED STATES
Latimer, Darin R., East Haven, CT, UNITED STATES
PA Horlick, Kenneth R. (U.S. corporation)
PI US 2004265888 A1 20041230
AI US 2004-872984 A1 20040621 (10)
RLI Continuation of Ser. No. US 2001-994311, filed on 26 Nov 2001, GRANTED, Pat. No. US 6773886 Continuation of Ser. No. US 2000-637751, filed on 11 Aug 2000, GRANTED, Pat. No. US 6383754 Continuation-in-part of Ser. No. US 2000-544713, filed on 6 Apr 2000, GRANTED, Pat. No. US 6261782
PRAI US 1999-148870P 19990813 (60)
DT Utility
FS APPLICATION
LREP NEEDLE & ROSENBERG, P.C., SUITE 1000, 999 PEACHTREE STREET, ATLANTA, GA, 30309-3915
CLMN Number of Claims: 126
ECL Exemplary Claim: 1
DRWN 3 Drawing Page(s)
LN.CNT 3697
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed is a method for the comprehensive analysis of nucleic acid samples and a detector composition for use in the method. The method, referred to as Binary Encoded Sequence Tags (BEST), involves generation of a set of nucleic acid fragments; adding an adaptor to the ends containing recognition site for cleavage at a site offset from the recognition site; cleaving the fragment to generate fragments having a plurality sticky ends; indexing of the fragments into sets based on the sequence of sticky ends. The fragments are indexed by adding a offset adaptor to newly generated ends. A different adaptor will be coupled to each different sticky end. The resulting fragments--which will have defined ends, be of equal lengths (in preferred embodiment), and a central sequence derived from the source nucleic acid molecule--are binary sequence tags. The binary sequence tags can be used and further

analyzed in numerous ways. For example, the binary sequence tags can be captured by hybridization and coupling, preferably by ligation, to a probe. The probe is preferably immobilized in an array or on sortable beads. One form of the BEST method, referred to as modification assisted analysis of binary sequence tags (MAABST), assesses modification of sequences in nucleic acid molecules by detecting differential cleavage based on the presence or absence of modification in the molecules.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 5 OF 27 USPATFULL on STN
AN 2004:327285 USPATFULL
TI Multiplex nucleic acid analysis using archived or fixed samples
IN Fan, Jian-Bing, San Diego, CA, UNITED STATES
Bibikova, Marina, San Diego, CA, UNITED STATES
PI US 2004259105 A1 20041223
AI US 2003-678608 A1 20031003 (10)
PRAI US 2002-416118P 20021003 (60)
DT Utility
FS APPLICATION
LREP McDERMOTT, WILL & EMERY, 7th Floor, 4370 La Jolla Village Drive, San Diego, CA, 92122
CLMN Number of Claims: 124
ECL Exemplary Claim: 1
DRWN 38 Drawing Page(s)
LN.CNT 6334
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention is directed to compositions and methods for multiplex analyses of nucleic acids from archival tissues.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 6 OF 27 USPATFULL on STN
AN 2004:314433 USPATFULL
TI Methods and reagents for profiling quantities of nucleic acids
IN Yakhini, Zohar, Ramat HaSharon, ISRAEL
Sampson, Jeffrey R., San Francisco, CA, UNITED STATES
Kronick, Mel N., Palo Alto, CA, UNITED STATES
Myerson, Joel, Berkeley, CA, UNITED STATES
Tsalenko, Anya, Chicago, IL, UNITED STATES
PI US 2004248104 A1 20041209
AI US 2003-455198 A1 20030605 (10)
DT Utility
FS APPLICATION
LREP AGILENT TECHNOLOGIES, INC., Legal Department, DL429, Intellectual Property Administration, P.O. Box 7599, Loveland, CO, 80537-0599
CLMN Number of Claims: 45
ECL Exemplary Claim: 1
DRWN 6 Drawing Page(s)
LN.CNT 2222
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods and reagents are disclosed for quantitatively analyzing a set of target nucleic acid sequences. In the method a unique set of oligonucleotide probe precursors is hybridized to the target nucleic acid sequences to produce hybrids. The hybrids are processed to alter the mass of each of the oligonucleotide probe precursors in the hybrids in a target sequence-mediated reaction to produce oligonucleotide products, each of which has a unique mass that is not a result of the presence of a mass tag in the oligonucleotide product. The processing of the hybrids may involve polymerase extension or ligation. The products are analyzed by means of mass spectrometry and the results are related to the amount of the target nucleic acid sequences in the set. Kits for carrying out the above methods are also disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 7 OF 27 USPATFULL on STN
AN 2004:267711 USPATFULL
TI Methods for determining protein and peptide terminal sequences
IN Schneider, Luke V., Half Moon Bay, CA, UNITED STATES
Hall, Michael P., Hayward, CA, UNITED STATES
Petesch, Robert, Newark, CA, UNITED STATES
PI US 2004209251 A1 20041021
AI US 2001-33303 A1 20011019 (10)
PRAI US 2000-242165P 20001019 (60)
US 2000-242398P 20001019 (60)
DT Utility
FS APPLICATION
LREP James C. Scheller, Jr., BLAKELY, SOKOLOFF, TAYLOR & ZAFMAN LLP, 7th Floor, 12400 Wilshire Boulevard, Los Angeles, CA, 90025
CLMN Number of Claims: 114
ECL Exemplary Claim: 1
DRWN 39 Drawing Page(s)
LN.CNT 3924
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods and apparatuses for deriving the sequence of an oligomer. In one exemplary method for deriving the sequence of a polypeptide, a predetermined set of mass/charge values for amino acid sequences is stored. An abundance value from mass spectrum data for each mass/charge value in the predetermined set is determined to produce a plurality of abundance values. A first ranking, based on the plurality of abundance values, is calculated for each sequence of a set of amino acid sequences having a first number of amino acids. A second ranking, based on the plurality of abundance values, for each sequence of a set of amino acid sequences having a second number of amino acids is calculated. A cumulative ranking, based on the first ranking and the second ranking, is calculated for each sequence of a set of amino acid sequences having at least the second number of amino acids.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 8 OF 27 USPATFULL on STN
AN 2004:158565 USPATFULL
TI Multiplex nucleic acid reactions
IN Chee, Mark, Del Mar, CA, UNITED STATES
Fan, Jian-Bing, San Diego, CA, UNITED STATES
Gunderson, Kevin, Encinitas, CA, UNITED STATES
PI US 2004121364 A1 20040624
AI US 2003-620852 A1 20030715 (10)
RLI Continuation-in-part of Ser. No. US 2002-194958, filed on 12 Jul 2002, PENDING Continuation-in-part of Ser. No. US 2002-177727, filed on 20 Jun 2002, PENDING Continuation-in-part of Ser. No. US 2001-931285, filed on 16 Aug 2001, PENDING Continuation-in-part of Ser. No. US 2001-915231, filed on 24 Jul 2001, PENDING Continuation-in-part of Ser. No. US 2001-779376, filed on 7 Feb 2001, PENDING Continuation-in-part of Ser. No. WO 2001-US4056, filed on 7 Feb 2001, PENDING
PRAI US 2002-396237P 20020715 (60)
US 2001-341827P 20011217 (60)
US 2001-336958P 20011203 (60)
US 2001-311271P 20010809 (60)
US 2001-305118P 20010712 (60)
US 2001-297609P 20010611 (60)
US 2000-234143P 20000921 (60)
US 2000-234732P 20000922 (60)
US 2000-180810P 20000207 (60)
US 2000-234732P 20000922 (60)
US 2000-180810P 20000207 (60)

DT Utility
FS APPLICATION
LREP David A. Gay, McDERMOTT, WILL & EMERY, 7th Floor, 4370 La Jolla Village Drive, San Diego, CA, 92122
CLMN Number of Claims: 103
ECL Exemplary Claim: 1
DRWN 28 Drawing Page(s)
LN.CNT 5892
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention is directed to a variety of multiplexing methods used to amplify and/or genotype a variety of samples simultaneously. The invention provides a method of detecting a target sequence. The method consists of: (a) contacting a first and second probe with a target sequence under conditions where complementary probes form a hybridization complex with the target sequence, the first probe comprising an upstream universal priming site and a target-specific sequence, the second probe comprising a downstream universal priming site and a target-specific sequence, wherein one of the first or second probes comprise an adapter sequence; (b) extending the first or second probe of the hybridization complex to form a modified probe; (c) amplifying the modified probe to form an amplicon, and (d) detecting the amplicon. A method of detecting the relative amounts of two or more target sequences is also provided. The method consists of: (a) contacting a first and a second probe with first and second target sequences in an initial population under conditions where complementary probes form a hybridization complex with the target sequences, the first and second probes comprising a universal priming site, an adapter sequence and a target-specific sequence; (b) linearly amplifying the first and second probes forming the hybridization complex to produce first and second amplicons having distinctive adapter sequences, and (c) determining a relative amount of the first and second amplicons distinguishable by the adapter sequence, wherein the relative amount of the amplicons is indicative of the relative amounts of the first and second target sequences in the initial population. Further provided is a method of amplifying a target sequence to produce a signal within a dynamic range of a detection assay. The method consists of: (a) hybridizing a target-specific probe having an upstream universal priming site (UUP), a downstream universal priming site (DUP) and an adapter sequence with a set of differential primers, the set of differential primers comprising an upstream primer and first and second downstream primers, the second downstream primer having a lower Tm compared to the upstream primer and the first downstream primer; (b) amplifying the probe with the set of differential primers for two or more cycles of enzymatic polymerization; (c) increasing hybridization stringency to suppress hybridization of the second downstream primer, and (d) amplifying the probe from the upstream and the first downstream primers of the set for at least one cycle of enzymatic polymerization, wherein differential signals of amplicons produced from amplification of the first or the second downstream primers fall within a dynamic range of a detection assay.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 9 OF 27 USPATFULL on STN
AN 2004:133299 USPATFULL
TI DIRECT MULTIPLEX CHARACTERIZATION OF GENOMIC DNA
IN Willis, Thomas D., San Francisco, CA, UNITED STATES
Hardenbol, Paul, Los Altos, CA, UNITED STATES
Jain, Maneesh, Menlo Park, CA, UNITED STATES
Stolc, Viktor, Cupertino, CA, UNITED STATES
Ronaghi, Mostafa, Palo Alto, CA, UNITED STATES
Davis, Ronald W., Palo Alto, CA, UNITED STATES
PI US 2004101835 A1 20040527
US 6858412 B2 20050222

AI US 2001-999362 A1 20011024 (9)
PRAI US 2000-242901P 20001024 (60)
DT Utility
FS APPLICATION
LREP DORSEY & WHITNEY LLP, Suite 3400, Four Embarcadero Center, San Francisco, CA, 94111-4187
CLMN Number of Claims: 47
ECL Exemplary Claim: 1
DRWN 18 Drawing Page(s)
LN.CNT 4346
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention is directed to novel methods of multiplexing nucleic acid reactions, including amplification, detection and genotyping. The invention relies on the use of precircle probes that are circularized in the presence of the corresponding target nucleic acids, cleaved, and then amplified.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 10 OF 27 USPATFULL on STN
AN 2004:44530 USPATFULL
TI Method of DNA sequencing using cleavable tags
IN Fischer, Steven M., Hayward, CA, UNITED STATES
PI US 2004033522 A1 20040219
AI US 2003-611409 A1 20030630 (10)
RLI Continuation of Ser. No. US 2001-896299, filed on 29 Jun 2001, GRANTED, Pat. No. US 6613523
DT Utility
FS APPLICATION
LREP AGILENT TECHNOLOGIES, INC., INTELLECTUAL PROPERTY ADMINISTRATION, LEGAL DEPT., P.O. BOX 7599, M/S DL429, LOVELAND, CO, 80537-0599
CLMN Number of Claims: 20
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 1008
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides novel systems for sequencing nucleic acid molecules using dNTPs that are 3' end labeled with cleavable tags that block further extension and uniquely identify the bases to which they are attached. Removal of the tags liberates the 3' ends of the extension products for further extension. In related embodiments, oligonucleotides containing sequence-related cleavable tags are employed in a ligation reaction to determine the sequence of a particular DNA sample.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 11 OF 27 USPATFULL on STN
AN 2003:300266 USPATFULL
TI Multiplex nucleic acid reactions
IN Shen, Min-Jui Richard, San Diego, CA, UNITED STATES
Oliphant, Arnold, Poway, CA, UNITED STATES
Butler, Scott L., San Diego, CA, UNITED STATES
Stuelpnagel, John R., Encinitas, CA, UNITED STATES
Chee, Mark S., Del Mar, CA, UNITED STATES
Kuhn, Kenneth M., San Diego, CA, UNITED STATES
Fan, Jian-Bing, San Diego, CA, UNITED STATES
PI US 2003211489 A1 20031113
AI US 2002-177727 A1 20020620 (10)
PRAI US 2000-234143P 20000921 (60)
US 2000-234732P 20000922 (60)
US 2001-311271P 20010809 (60)
US 2001-336958P 20011203 (60)
US 2001-305118P 20010712 (60)
US 2001-341827P 20011217 (60)

DT Utility
FS APPLICATION
LREP Robin M. Silva, Esq., DORSEY & WHITNEY LLP, Suite 3400, Four Embarcadero Center, San Francisco, CA, 94111-4187
CLMN Number of Claims: 11
ECL Exemplary Claim: 1
DRWN 14 Drawing Page(s)
LN.CNT 4352
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention is directed to a variety of multiplexing methods used to amplify and/or genotype a variety of samples simultaneously.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 12 OF 27 USPATFULL on STN
AN 2003:213675 USPATFULL
TI Applications of parallel genomic analysis
IN Strathmann, Michael Paul, Mukilteo, WA, UNITED STATES
PI US 2003148313 A1 20030807
AI US 2002-209676 A1 20020730 (10)
RLI Continuation-in-part of Ser. No. US 1999-427834, filed on 26 Oct 1999, GRANTED, Pat. No. US 6480791
DT Utility
FS APPLICATION
LREP Michael Strathmann, 5300 Harbour Pointe Blvd. 302-B, Mukilteo, WA, 98275
CLMN Number of Claims: 42
ECL Exemplary Claim: 1
DRWN 8 Drawing Page(s)
LN.CNT 5090
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides parallel methods for determining nucleotide sequences of polynucleotides associated with sample tags. Applications of sequence information acquired by these methods are also provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 13 OF 27 USPATFULL on STN
AN 2003:159287 USPATFULL
TI Multiplex nucleic acid reactions
IN Oliphant, Arnold, Poway, CA, UNITED STATES
Stuelpnagel, John R., Encinitas, CA, UNITED STATES
Chee, Mark S., Del Mar, CA, UNITED STATES
Butler, Scott L., San Diego, CA, UNITED STATES
PI US 2003108900 A1 20030612
AI US 2002-194958 A1 20020712 (10)
PRAI US 2001-311271P 20010809 (60)
US 2001-336958P 20011203 (60)
US 2001-305118P 20010712 (60)
US 2001-341827P 20011217 (60)
DT Utility
FS APPLICATION
LREP Robin M. Silva, Esq., DORSEY & WHITNEY LLP, Suite 3400, Four Embarcadero Center, San Francisco, CA, 94111-4187
CLMN Number of Claims: 14
ECL Exemplary Claim: 1
DRWN 16 Drawing Page(s)
LN.CNT 4371
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention is directed to a variety of multiplexing methods used to amplify and/or genotype a variety of samples simultaneously.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 14 OF 27 USPATFULL on STN
AN 2003:120073 USPATFULL
TI Binary encoded sequence tags
IN Kaufman, Joseph C., Hamden, CT, UNITED STATES
Roth, Matthew E., Branford, CT, UNITED STATES
Lizardi, Paul M., Wallingford, CT, UNITED STATES
Feng, Li, Hamden, CT, UNITED STATES
Latimer, Darin R., East Haven, CT, UNITED STATES
PA Yale University (U.S. corporation)
PI US 2003082556 A1 20030501
US 6773886 B2 20040810
AI US 2001-994311 A1 20011126 (9)
RLI Continuation of Ser. No. US 2000-637751, filed on 11 Aug 2000, PENDING
Continuation-in-part of Ser. No. US 2000-544713, filed on 6 Apr 2000, PATENTED
PRAI US 1999-148870P 19990813 (60)
DT Utility
FS APPLICATION
LREP NEEDLE & ROSENBERG, P.C., Suite 1200, The Candler Building, 127 Peachtree Street, N.E., Atlanta, GA, 30303-1811
CLMN Number of Claims: 126
ECL Exemplary Claim: 1
DRWN 3 Drawing Page(s)
LN.CNT 3686
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed is a method for the comprehensive analysis of nucleic acid samples and a detector composition for use in the method. The method, referred to as Binary Encoded Sequence Tags (BEST), involves generation of a set of nucleic acid fragments; adding an adaptor to the ends containing recognition site for cleavage at a site offset from the recognition site; cleaving the fragment to generate fragments having a plurality sticky ends; indexing of the fragments into sets based on the sequence of sticky ends. The fragments are indexed by adding a offset adaptor to newly generated ends. A different adaptor will be coupled to each different sticky end. The resulting fragments--which will have defined ends, be of equal lengths (in preferred embodiment), and a central sequence derived from the source nucleic acid molecule--are binary sequence tags. The binary sequence tags can be used and further analyzed in numerous ways. For example, the binary sequence tags can be captured by hybridization and coupling, preferably by ligation, to a probe. The probe is preferably immobilized in an array or on sortable beads. One form of the BEST method, referred to as modification assisted analysis of binary sequence tags (MAABST), assesses modification of sequences in nucleic acid molecules by detecting differential cleavage based on the presence or absence of modification in the molecules.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 15 OF 27 USPATFULL on STN
AN 2003:10591 USPATFULL
TI Method of DNA sequencing using cleavable tags
IN Fischer, Steven M., Hayward, CA, UNITED STATES
PI US 2003008285 A1 20030109
US 6613523 B2 20030902
AI US 2001-896299 A1 20010629 (9)
DT Utility
FS APPLICATION
LREP AGILENT TECHNOLOGIES, INC., Legal Department, DL429, Intellectual Property Administration, P. O. Box 7599, Loveland, CO, 80537-0599
CLMN Number of Claims: 20
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 1009
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention provides novel systems for sequencing nucleic acid molecules using dNTPs that are 3' end labeled with cleavable tags that block further extension and uniquely identify the bases to which they are attached. Removal of the tags liberates the 3' ends of the extension products for further extension. In related embodiments, oligonucleotides containing sequence-related cleavable tags are employed in a ligation reaction to determine the sequence of a particular DNA sample.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 16 OF 27 USPATFULL on STN
AN 2002:343903 USPATFULL
TI Apparatus and method for separating and purifying polynucleotides
IN Gjerde, Douglas T., Saratoga, CA, UNITED STATES
Hanna, Christopher P., Somerville, MA, UNITED STATES
Taylor, Paul D., Palo Alto, CA, UNITED STATES
Legendre, Benjamin L., JR., Belleview, NE, UNITED STATES
Haefele, Robert M., Palo Alto, CA, UNITED STATES
PI US 2002197629 A1 20021226
AI US 2002-121552 A1 20020412 (10)
RLI Division of Ser. No. US 1999-318407, filed on 25 May 1999, GRANTED, Pat. No. US 6265168
PRAI US 1998-103313P 19981006 (60)
US 1999-117211P 19990125 (60)
US 1999-117178P 19990125 (60)
US 1999-119945P 19990212 (60)
US 1999-123301P 19990303 (60)
US 1999-129838P 19990416 (60)
US 1999-130700P 19990423 (60)
DT Utility
FS APPLICATION
LREP JOHN F. BRADY, TRANSGENOMIC, INC., 2032 CONCOURSE DRIVE, SAN JOSE, CA, 95131
CLMN Number of Claims: 44
ECL Exemplary Claim: 1
DRWN 16 Drawing Page(s)
LN.CNT 2528
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method for removing a target DNA fragment having a predetermined base-pair length from a mixture of DNA fragments comprises the following steps. A mixture of DNA fragments which may contain the target DNA fragments is applied to a separation column containing media having a nonpolar, nonporous surface, the mixture of DNA fragments being in a first solvent mixture containing a counterion and a DNA binding concentration of driving solvent in a cosolvent. The target DNA fragments are separated from the media by contacting it with a second solvent solution containing a counterion and a concentration of driving solvent in cosolvent which has been predetermined to remove DNA fragments having the target DNA fragment base pair length from the media. The target DNA fragments can be collected and optionally amplified. When the method is being applied to collect a putative fragment, if present, no DNA fragments having the base pair length of the target DNA could be present in the mixture. Alternatively, DNA fragments having the base pair length of the target DNA are present in the mixture. The disclosure also describes an ambient or low pressure device for separating polynucleotide fragments from a mixture of polynucleotide fragments comprises a tube having an upper solution input chamber, a lower eluant receiving chamber, and a fixed unit of separation media supported therein. The separation media has nonpolar separation surfaces which are free from multivalent cations which would react with counterion to form an insoluble polar coating on

the surface of the separation media.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 17 OF 27 USPATFULL on STN
AN 2002:322437 USPATFULL
TI Method and reagents for analyzing the nucleotide sequence of nucleic acids
IN Sampson, Jeffrey R., Burlingame, CA, UNITED STATES
Myerson, Joel, Berkeley, CA, UNITED STATES
Tsalenko, Anna M., Chicago, IL, UNITED STATES
Sampas, Nicholas M., San Jose, CA, UNITED STATES
Webb, Peter G., Menlo Park, CA, UNITED STATES
Yakhini, Zohar H., Zikhron Ya'Acov, ISRAEL
PI US 2002182601 A1 20021205
AI US 2001-836012 A1 20010417 (9)
RLI Continuation-in-part of Ser. No. US 1998-112437, filed on 9 Jul 1998, GRANTED, Pat. No. US 6218118
DT Utility
FS APPLICATION
LREP AGILENT TECHNOLOGIES, Legal Department, DL429, Intellectual Property Administration, P.O. Box 58043, Santa Clara, CA, 95052-8043
CLMN Number of Claims: 80
ECL Exemplary Claim: 1
DRWN 13 Drawing Page(s)
LN.CNT 3253
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods and reagents are disclosed which provide for more sensitive, more accurate and higher through-put analyses of target nucleic acid sequences. The methods and reagents of the present invention may be generically applied to generally any target nucleic acid sequence and do not require a priori information about the presence, location or identity of mutations in the target nucleic acid sequence. The reagents of the invention are mixtures of oligonucleotide precursors having a high level of coverage and mass number complexity, and also having tags analyzable by mass spectrometry which are covalently linked to the precursors through cleavable bonds. A method is also disclosed for analyzing a target nucleic acid sequence employing the mixtures of oligonucleotide precursors having tags analyzable by mass spectrometry covalently linked to the oligonucleotide precursors through cleavable bonds, and chemical or enzymatic assays to alter the mass of the oligonucleotide precursors prior to mass spectral analysis. The enzymatic assay may be a polymerase extension assay or a ligation-based assay. The kits for carrying out the methods of the invention are also disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 18 OF 27 USPATFULL on STN
AN 2002:307838 USPATFULL
TI Mass defect labeling for the determination of oligomer sequences
IN Schneider, Luke V., Half Moon Bay, CA, UNITED STATES
Hall, Michael P., San Carlos, CA, UNITED STATES
Petesch, Robert, Newark, CA, UNITED STATES
PA Target Discovery, San Carlos, CA, UNITED STATES, 94070 (U.S. corporation)
PI US 2002172961 A1 20021121
US 6962818 B2 20051108
AI US 2001-35349 A1 20011019 (10)
PRAI US 2000-242165P 20001019 (60)
US 2000-242398P 20001019 (60)
DT Utility
FS APPLICATION
LREP TOWNSEND AND TOWNSEND AND CREW, LLP, TWO EMBARCADERO CENTER, EIGHTH

FLOOR, SAN FRANCISCO, CA, 94111-3834
CLMN Number of Claims: 50
ECL Exemplary Claim: 1
DRWN 32 Drawing Page(s)
LN.CNT 3568
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Mass tagging methods are provided that lead to mass spectrometer detection sensitivities and molecular discriminations that are improved over other methods. In particular the methods are useful for discriminating tagged molecules and fragments of molecules from chemical noise in the mass spectrum. These mass tagging methods are useful for oligomer sequencing, determining the relative abundances of molecules from different samples, and identifying individual molecules or chemical processing steps in combinatorial chemical libraries. The methods provided are useful for the simultaneous analysis of multiple molecules and reaction mixtures by mass spectrometric methods.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 19 OF 27 USPATFULL on STN
AN 2002:198549 USPATFULL
TI Fixed address analysis of sequence tags
IN Lizardi, Paul M., Wallingford, CT, UNITED STATES
Roth, Matthew E., Branford, CT, UNITED STATES
Feng, Li, Hamden, CT, UNITED STATES
Guerra, Cesar E., Guilford, CT, UNITED STATES
Weber, Shane C., Woodbridge, CT, UNITED STATES
Kaufman, Joseph C., Hamden, CT, UNITED STATES
Latimer, Darin R., East Haven, CT, UNITED STATES
PA Yale University (U.S. corporation)
PI US 2002106649 A1 20020808
US 6677121 B2 20040113
AI US 2001-855793 A1 20010515 (9)
RLI Continuation of Ser. No. US 2000-544713, filed on 6 Apr 2000, PATENTED
PRAI US 1999-127932P 19990406 (60)
DT Utility
FS APPLICATION
LREP Robert A. Hodges, NEEDLE & ROSENBERG, P.C., The Candler Building, Suite 1200, 127 Peachtree Street, N.E., Atlanta, GA, 30303-1811
CLMN Number of Claims: 154
ECL Exemplary Claim: 1
DRWN 5 Drawing Page(s)
LN.CNT 4340
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed is a method for the comprehensive analysis of nucleic acid samples and a detector composition for use in the method. The method, referred to as Fixed Address Analysis of Sequence Tags (FAAST), involves generation of a set of nucleic acid fragments having a variety of sticky end sequences; indexing of the fragments into sets based on the sequence of sticky ends; associating a detector sequence with the fragments; sequence-based capture of the indexed fragments on a detector array; and detection of the fragment labels. Generation of the multiple sticky end sequences is accomplished by incubating the nucleic acid sample with one or more nucleic acid cleaving reagents. The indexed fragments are captured by hybridization and coupling, preferably by ligation, to a probe. The method allows a complex sample of nucleic acid to be quickly and easily cataloged in a reproducible and sequence-specific manner. One form of the method allows determination of associations, in a nucleic acid molecule, of different combinations of known or potential sequences. Another form of the method assesses modification of sequences in nucleic acid molecules by basing cleavage of the molecules on the presence or absence of modification.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 20 OF 27 USPATFULL on STN
AN 2002:43173 USPATFULL
TI Methods for preparing conjugates
IN Dellinger, Douglas J., Sunnyvale, CA, UNITED STATES
Myerson, Joel, Berkeley, CA, UNITED STATES
Fulcrand, Geraldine, Sunnyvale, CA, UNITED STATES
Ilsley, Diane D., San Jose, CA, UNITED STATES
PI US 2002025539 A1 20020228
US 6743585 B2 20040601
AI US 2001-981580 A1 20011017 (9)
RLI Division of Ser. No. US 1999-397526, filed on 16 Sep 1999, PENDING
DT Utility
FS APPLICATION
LREP AGILENT TECHNOLOGIES, INC., Legal Department, DL429, Intellectual Property Administration, P. O. Box 7599, Loveland, CO, 80537-0599
CLMN Number of Claims: 45
ECL Exemplary Claim: 1
DRWN 2 Drawing Page(s)
LN.CNT 1750
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods are disclosed for conjugating one moiety to another moiety. In the method the moieties are reacted with one another in a protic solvent. Reaction between the moieties and the protic solvent during the conjugating is negligible or reversible. A stable bond is formed between the moieties to produce a product that is not subject to β-elimination at elevated pH. Usually, one of the moieties comprises an unsaturation between two carbon atoms. One of the carbon atoms is or becomes an electrophile during the conjugating. The other of the moieties comprises a functionality reactive with the electrophile carbon atom to form a product that comprises the unsaturation. Compounds comprising both of the moieties as well as precursor molecules are also disclosed. Methods are also disclosed for determining an analyte in a sample employing compounds as described above.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 21 OF 27 USPATFULL on STN
AN 2002:298463 USPATFULL
TI Parallel methods for genomic analysis
IN Strathmann, Michael P., 1674 Euclid Ave., Berkeley, CA, United States 94709
PI US 6480791 B1 20021112
AI US 1999-427834 19991026 (9)
PRAI US 1998-105914P 19981028 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Brusca, John S.; Assistant Examiner: Moran, Marjorie A.
LREP McCutchen, Doyle, Brown & Enersen, LLP, Shuster, Michael J.
CLMN Number of Claims: 30
ECL Exemplary Claim: 1
DRWN 10 Drawing Figure(s); 8 Drawing Page(s)
LN.CNT 4843
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides parallel methods for determining nucleotide sequences and physical maps of polynucleotides associated with sample tags. This information can be used to determine the chromosomal locations of sample-tagged polynucleotides. In one embodiment, the polynucleotides are derived from genomic DNA coupled to insertion elements. As a result, the invention also provides parallel methods for locating the integration sites of insertion elements in the genome.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 22 OF 27 USPATFULL on STN
AN 2002:174707 USPATFULL
TI Apparatus and method for separating and purifying polynucleotides
IN Gjerde, Douglas T., Saratoga, CA, United States
Hanna, Christopher P., Somerville, MA, United States
Taylor, Paul D., Palo Alto, CA, United States
Legendre, Jr., Benjamin L., Belleview, NE, United States
Haefele, Robert M., Palo Alto, CA, United States
PA Transgenomic, Inc., San Jose, CA, United States (U.S. corporation)
PI US 6419824 B1 20020716
AI US 2001-912568 20010724 (9)
RLI Division of Ser. No. US 1999-318407, filed on 25 May 1999, now patented, Pat. No. US 6265168 Continuation-in-part of Ser. No. US 1999-311116, filed on 13 May 1999, now patented, Pat. No. US 6218153 Continuation-in-part of Ser. No. US 1998-183573, filed on 30 Oct 1998, now abandoned Continuation-in-part of Ser. No. US 1998-183450, filed on 30 Oct 1998, now patented, Pat. No. US 5997742 Continuation-in-part of Ser. No. US 1998-183123, filed on 30 Oct 1998, now patented, Pat. No. US 6056877 Continuation-in-part of Ser. No. US 1998-183047, filed on 30 Oct 1998, now patented, Pat. No. US 6066258 Continuation-in-part of Ser. No. US 1998-129105, filed on 4 Aug 1998, now patented, Pat. No. US 6024878 Continuation-in-part of Ser. No. US 1998-81039, filed on 18 May 1998, now patented, Pat. No. US 5972222 Continuation-in-part of Ser. No. US 1998-58580, filed on 10 Apr 1998, now abandoned Continuation-in-part of Ser. No. US 1998-58337, filed on 10 Apr 1998, now abandoned Continuation-in-part of Ser. No. US 1998-39061, filed on 13 Mar 1998
PRAI US 1999-130700P 19990423 (60)
US 1999-129838P 19990416 (60)
US 1999-123301P 19990303 (60)
US 1999-119945P 19990212 (60)
US 1999-117178P 19990125 (60)
US 1999-117211P 19990125 (60)
US 1998-103313P 19981006 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Therkorn, Ernest G.
LREP Walker, William B.
CLMN Number of Claims: 13
ECL Exemplary Claim: 10
DRWN 32 Drawing Figure(s); 16 Drawing Page(s)
LN.CNT 2441
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The disclosure describes an ambient or low pressure device for separating polynucleotide fragments from a mixture of polynucleotide fragments comprises a tube having an upper solution input chamber, a lower eluant receiving chamber, and a fixed unit of separation media supported therein. The separation media has nonpolar separation surfaces which are free from multivalent cations which would react with counterion to form an insoluble polar coating on the surface of the separation media.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 23 OF 27 USPATFULL on STN
AN 2002:136767 USPATFULL
TI Analysis of sequence tags with hairpin primers
IN Lizardi, Paul M., Wallingford, CT, United States
Latimer, Darin R., East Haven, CT, United States
PA Yale University, New Haven, CT, United States (U.S. corporation)
PI US 6403319 B1 20020611
AI US 2000-637384 20000811 (9)
RLI Continuation-in-part of Ser. No. US 2000-544713, filed on 6 Apr 2000,

now patented, Pat. No. US 6261782
PRAI US 1999-148870P 19990813 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Needle & Rosenberg, P.C.
CLMN Number of Claims: 106
ECL Exemplary Claim: 1
DRWN 7 Drawing Figure(s); 7 Drawing Page(s)
LN.CNT 3134
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed is a method for the comprehensive analysis of nucleic acid samples and a detector composition for use in the method. The method involves amplifying nucleic acid fragments of interest using a primer that can form a hairpin structure; sequence-based coupling of the amplified fragments to detector probes; and detection of the coupled fragments. The amplified fragments are coupled by hybridization and coupling, preferably by ligation, to detector probes. A hairpin structure formed at the end of the amplified fragments facilitates coupling of the fragments to the probes. The method allows detection of the fragments where detection provides some sequence information for the fragments. The method allows a complex sample of nucleic acid to be quickly and easily cataloged in a reproducible and sequence-specific manner. The method can also be used to detect amplified fragments having a known sequence.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 24 OF 27 USPATFULL on STN
AN 2002:102268 USPATFULL
TI Binary encoded sequence tags
IN Kaufman, Joseph C., Hamden, CT, United States
Roth, Matthew E., Branford, CT, United States
Lizardi, Paul M., Wallingford, CT, United States
Feng, Li, Hamden, CT, United States
Latimer, Darin R., East Haven, CT, United States
PA Yale University, United States (U.S. corporation)
Agilix Corporation, United States (U.S. corporation)
PI US 6383754 B1 20020507
AI US 2000-637751 20000811 (9)
RLI Continuation-in-part of Ser. No. US 2000-544713, filed on 6 Apr 2000, now patented, Pat. No. US 6261782
PRAI US 1999-148870P 19990813 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Needle & Rosenberg, P.C.
CLMN Number of Claims: 131
ECL Exemplary Claim: 1
DRWN 3 Drawing Figure(s); 3 Drawing Page(s)
LN.CNT 3871
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed is a method for the comprehensive analysis of nucleic acid samples and a detector composition for use in the method. The method, referred to as Binary Encoded Sequence Tags (BEST), involves generation of a set of nucleic acid fragments; adding an adaptor to the ends containing recognition site for cleavage at a site offset from the recognition site; cleaving the fragment to generate fragments having a plurality sticky ends; indexing of the fragments into sets based on the sequence of sticky ends. The fragments are indexed by adding a offset adaptor to newly generated ends. A different adaptor will be coupled to each different sticky end. The resulting fragments--which will have defined ends, be of equal lengths (in preferred embodiment), and a central sequence derived from the source nucleic acid molecule--are

binary sequence tags. The binary sequence tags can be used and further analyzed in numerous ways. For example, the binary sequence tags can be captured by hybridization and coupling, preferably by ligation, to a probe. The probe is preferably immobilized in an array or on sortable beads. One form of the BEST method, referred to as modification assisted analysis of binary sequence tags (MAABST), assesses modification of sequences in nucleic acid molecules by detecting differential cleavage based on the presence or absence of modification in the molecules.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 25 OF 27 USPATFULL on STN
AN 2001:116774 USPATFULL
TI Apparatus and method for separating and purifying polynucleotides
IN Gjerde, Douglas T., Saratoga, CA, United States
Hanna, Christopher P., Somerville, MA, United States
Taylor, Paul D., Palo Alto, CA, United States
Legendre, Jr., Benjamin L., Belleview, NE, United States
Haefele, Robert M., Palo Alto, CA, United States
PA Transgenomic, Inc., San Jose, CA, United States (U.S. corporation)
PI US 6265168 B1 20010724
AI US 1999-318407 19990525 (9)
PRAI US 1999-130700P 19990423 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Chakrabarti, Arun Kr.
LREP Walker, William B.
CLMN Number of Claims: 49
ECL Exemplary Claim: 1
DRWN 32 Drawing Figure(s); 16 Drawing Page(s)
LN.CNT 2760
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method for removing a target DNA fragment having a predetermined base-pair length from a mixture of DNA fragments comprises the following steps. A mixture of DNA fragments which may contain the target DNA fragments is applied to a separation column containing media having a nonpolar, nonporous surface, the mixture of DNA fragments being in a first solvent mixture containing a counterion and a DNA binding concentration of driving solvent in a cosolvent. The target DNA fragments are separated from the media by contacting it with a second solvent solution containing a counterion and a concentration of driving solvent in cosolvent which has been predetermined to remove DNA fragments having the target DNA fragment base pair length from the media. The target DNA fragments can be collected and optionally amplified. When the method is being applied to collect a putative fragment, if present, no DNA fragments having the base pair length of the target DNA could be present in the mixture. Alternatively, DNA fragments having the base pair length of the target DNA are present in the mixture. The disclosure also describes an ambient or low pressure device for separating polynucleotide fragments from a mixture of polynucleotide fragments comprises a tube having an upper solution input chamber, a lower eluant receiving chamber, and a fixed unit of separation media supported therein. The separation media has nonpolar separation surfaces which are free from multivalent cations which would react with counterion to form an insoluble polar coating on the surface of the separation media.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 26 OF 27 USPATFULL on STN

AN 2001:112050 USPATFULL
TI Fixed address analysis of sequence tags
IN Lizardi, Paul M., Wallingford, CT, United States
Roth, Matthew E., Branford, CT, United States
Feng, Li, Hamden, CT, United States
Guerra, Cesar E., Guilford, CT, United States
Weber, Shane C., Woodbridge, CT, United States
Kaufman, Joseph C., Hamden, CT, United States
Latimer, Darin R., East Haven, CT, United States
PA Yale University, New Haven, CT, United States (U.S. corporation)
PI US 6261782 B1 20010717
AI US 2000-544713 20000406 (9)
PRAI US 1999-127932P 19990406 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Needle & Rosenberg, P.C.
CLMN Number of Claims: 154
ECL Exemplary Claim: 1
DRWN 5 Drawing Figure(s); 5 Drawing Page(s)
LN.CNT 4505
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed is a method for the comprehensive analysis of nucleic acid samples and a detector composition for use in the method. The method, referred to as Fixed Address Analysis of Sequence Tags (FAAST), involves generation of a set of nucleic acid fragments having a variety of sticky end sequences; indexing of the fragments into sets based on the sequence of sticky ends; associating a detector sequence with the fragments; sequence-based capture of the indexed fragments on a detector array; and detection of the fragment labels. Generation of the multiple sticky end sequences is accomplished by incubating the nucleic acid sample with one or more nucleic acid cleaving reagents. The indexed fragments are captured by hybridization and coupling, preferably by ligation, to a probe. The method allows a complex sample of nucleic acid to be quickly and easily cataloged in a reproducible and sequence-specific manner. One form of the method allows determination of associations, in a nucleic acid molecule, of different combinations of known or potential sequences. Another form of the method assesses modification of sequences in nucleic acid molecules by basing cleavage of the molecules on the presence or absence of modification.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L11 ANSWER 27 OF 27 USPATFULL on STN
AN 2001:55695 USPATFULL
TI Method and mixture reagents for analyzing the nucleotide sequence of nucleic acids by mass spectrometry
IN Sampson, Jeffrey R., Burlingame, CA, United States
Yakhini, Zohar H., Palo Alto, CA, United States
Webb, Peter G., Menlo Park, CA, United States
Sampas, Nicholas M., San Jose, CA, United States
Tsalenko, Anna M., Chicago, IL, United States
Myerson, Joel, Berkeley, CA, United States
PA Agilent Technologies, Inc., Palo Alto, CA, United States (U.S. corporation)
PI US 6218118 B1 20010417
AI US 1998-112437 19980709 (9)
DT Utility
FS Granted
EXNAM Primary Examiner: Horlick, Kenneth R.; Assistant Examiner: Siew, Jeffrey
CLMN Number of Claims: 70
ECL Exemplary Claim: 1
DRWN 26 Drawing Figure(s); 22 Drawing Page(s)
LN.CNT 2982

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Methods and reagents are disclosed which satisfy the need for more sensitive, more accurate and higher through-put analyses of target nucleic acid sequences. The methods and reagents may be generically applied to generally any target nucleic acid sequence and do not require a priori information about the presence, location or identity of mutations in the target nucleic acid sequence. The reagents of the invention are mixtures of natural and mass-modified oligonucleotide precursors having a high level of coverage and mass number complexity. A method is also disclosed for analyzing a target nucleic acid sequence employing the mixtures of natural and mass-modified oligonucleotide precursors and chemical or enzymatic assays to alter the mass of the oligonucleotide precursors prior to mass spectral analysis, generally via MALDI-TOF. The enzymatic assay may be a polymerase extension assay or a ligase assay. The kits for carrying out the methods of the invention are also disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

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